

## CLAIMS

What is claimed is:

1. An isolated nucleic acid probe for identifying an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Providencia stuartii* and *Serratia marcescens*, wherein the probe selectively hybridizes to a portion of the nucleic acid of SEQ ID NOS:1-8, or a complementary sequence thereof, respectively.
2. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of an *Escherichia coli* nucleic acid of SEQ ID NO:1, or a complementary sequence thereof.
3. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of a *Citrobacter freundii* nucleic acid of SEQ ID NO:2, or a complementary sequence thereof.
4. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of an *Enterobacter aerogenes* nucleic acid of SEQ ID NO:3, or a complementary sequence thereof.
5. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of an *Enterobacter cloacae* nucleic acid of SEQ ID NO:4, or a complementary sequence thereof.
6. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of a *Klebsiella oxytoca* nucleic acid of SEQ ID NO:5, or a complementary sequence thereof.

7. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of a *Klebsiella pneumoniae* nucleic acid of SEQ ID NO:6, or a complementary sequence thereof.

8. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of a *Providencia stuartii* nucleic acid of SEQ ID NO:7, or a complementary sequence thereof.

9. The isolated nucleic acid probe of Claim 1, wherein the probe selectively hybridizes to a portion of a *Serratia marcescens* nucleic acid of SEQ ID NO:8, or a complementary sequence thereof.

10. An isolated nucleic acid probe having a nucleic acid sequence of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, or SEQ ID NO:24, or a complementary sequence thereof.

11. A method of identifying in a sample an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Providencia stuartii* and *Serratia marcescens* comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NOS:1-8, or a complementary sequence thereof, respectively, the presence of hybridization with a nucleic acid indicating the identity of the respective species.

12. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:1, or a complementary sequence thereof, the presence of hybridization indicating *Escherichia coli* in the sample.

13. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:2, or a complementary sequence thereof, the presence of hybridization indicating *Citrobacter freundii* in the sample.

14. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:3, or a complementary sequence thereof, the presence of hybridization indicating *Enterobacter aerogenes* in the sample.

15. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:4, or a complementary sequence thereof, the presence of hybridization indicating *Enterobacter cloacae* in the sample.

16. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:5, or a complementary sequence thereof, the presence of hybridization indicating *Klebsiella oxytoca* in the sample.

17. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:6, or a complementary sequence thereof, the presence of hybridization indicating *Klebsiella pneumoniae* in the sample.

18. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:7, or a complementary sequence thereof, the presence of hybridization indicating *Providencia stuartii* in the sample.

19. The method of identifying an *Enterobacteriaceae* species of Claim 11, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NO:8, or a complementary sequence thereof, the presence of hybridization indicating *Serratia marcescens* in the sample.

20. An isolated nucleic acid probe capable of determining the quinolone resistance status of an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Providencia stuartii* and *Serratia marcescens*, wherein the probe selectively hybridizes to a portion of a nucleic acid of SEQ ID NOS:1-8, or a complementary sequence thereof, respectively.

21. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of an *Escherichia coli* nucleic acid of SEQ ID NO:1, or a complementary sequence thereof.

22. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of a *Citrobacter freundii* nucleic acid of SEQ ID NO:2, or a complementary sequence thereof.

23. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of an *Enterobacter aerogenes* nucleic acid of SEQ ID NO:3, or a complementary sequence thereof.

27

24. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of an *Enterobacter cloacae* nucleic acid of SEQ ID NO:4, or a complementary sequence thereof.

25. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of a *Klebsiella oxytoca* nucleic acid of SEQ ID NO:5, or a complementary sequence thereof.

26. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of a *Klebsiella pneumoniae* nucleic acid of SEQ ID NO:6, or a complementary sequence thereof.

27. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of a *Providencia stuartii* nucleic acid of SEQ ID NO:7, or a complementary sequence thereof.

28. The isolated nucleic acid probe of Claim 20, wherein the probe selectively hybridizes to a portion of a *Serratia marcescens* nucleic acid of SEQ ID NO:8, or a complementary sequence thereof.

29. An isolated nucleic acid probe having a nucleic acid sequence of SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, or SEQ ID NO:33, or a complementary sequence thereof.

30. A method of determining the quinolone resistance of an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Providencia stuartii* and *Serratia marcescens* in a sample, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NOS:9-16, or a complementary sequence thereof, respectively, the presence of hybridization with a nucleic acid indicating the quinolone resistance of the respective species.

31. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:9, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Escherichia coli* in the sample.

32. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:10, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Citrobacter freundii* in the sample.

33. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:11, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Enterobacter aerogenes* in the sample.

34. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:12, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Enterobacter cloacae* in the sample.

35. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:13, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Klebsiella oxytoca* in the sample.

36. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:14, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Klebsiella pneumoniae* in the sample.

37. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:15, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Providencia stuartii* in the sample.

38. The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:16, or a complementary sequence thereof, the presence of hybridization indicating quinolone resistance of the *Serratia marcescens* in the sample.